

RAW SEQUENCE LISTING

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Application Serial Number: 10/502,051
Source: PCT
Date Processed by STIC: 04/28/2006

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DATE: 04/28/2006

PATENT APPLICATION: US/10/502,051

TIME: 09:34:20

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Output Set: N:\CRF4\04282006\J502051.raw

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3 <110> APPLICANT: KADOWAKI, TAKASHI
4     YAMAUCHI, TOSHIMASA
5     KAMON, JUNJI
6     WAKI, HIRONORI
7     NAGAI, RYOZO
8     KIMURA, SATOSHI
9     TOMITA, MOTOO
11 <120> TITLE OF INVENTION: INSULIN RESISTANCE IMPROVING AGENT
13 <130> FILE REFERENCE: 256653US0PCT
15 <140> CURRENT APPLICATION NUMBER: 10/502,051
16 <141> CURRENT FILING DATE: 2004-07-30
18 <150> PRIOR APPLICATION NUMBER: PCT/JP02/07599
19 <151> PRIOR FILING DATE: 2002-07-26
21 <150> PRIOR APPLICATION NUMBER: JP 2002-23554
22 <151> PRIOR FILING DATE: 2002-01-31
24 <160> NUMBER OF SEQ ID NOS: 4
26 <170> SOFTWARE: PatentIn version 3.3
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 735
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
34 <220> FEATURE:
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (1)..(735)
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41 1          5          10          15
43 gac cag gaa acc acg act caa ggg ccc gga gtc ctg ctt ccc ctg ccc      96
44 Asp Gln Glu Thr Thr Thr Gln Gly Pro Gly Val Leu Leu Pro Leu Pro
45          20          25          30
47 aag ggg gcc tgc aca ggt tgg atg gcg ggc atc cca ggg cat ccg ggc      144
48 Lys Gly Ala Cys Thr Gly Trp Met Ala Gly Ile Pro Gly His Pro Gly
49          35          40          45
51 cat aat ggg gcc cca ggc cgt gat ggc aga gat ggc acc cct ggt gag      192
52 His Asn Gly Ala Pro Gly Arg Asp Gly Arg Asp Gly Thr Pro Gly Glu
53          50          55          60
55 aag ggt gag aaa gga gat cca ggt ctt att ggt cct aag gga gac atc      240
56 Lys Gly Glu Lys Gly Asp Pro Gly Leu Ile Gly Pro Lys Gly Asp Ile
57 65          70          75          80
59 ggt gaa acc gga gta ccc ggg gct gaa ggt ccc cga ggc ttt ccg gga      288
60 Gly Glu Thr Gly Val Pro Gly Ala Glu Gly Pro Arg Gly Phe Pro Gly
61          85          90          95

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63 atc caa ggc agg aaa gga gaa cct gga gaa ggt gcc tat gta tac cgc      336
64 Ile Gln Gly Arg Lys Gly Glu Pro Gly Glu Gly Ala Tyr Val Tyr Arg
65          100          105          110
67 tca gca ttc agt gtg gga ttg gag act tac gtt act atc ccc aac atg      384
68 Ser Ala Phe Ser Val Gly Leu Glu Thr Tyr Val Thr Ile Pro Asn Met
69          115          120          125
71 ccc att cgc ttt acc aag atc ttc tac aat cag caa aac cac tat gat      432
72 Pro Ile Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn His Tyr Asp
73          130          135          140
75 ggc tcc act ggt aaa ttc cac tgc aac att cct ggg ctg tac tac ttt      480
76 Gly Ser Thr Gly Lys Phe His Cys Asn Ile Pro Gly Leu Tyr Tyr Phe
77 145          150          155          160
79 gcc tac cac atc aca gtc tat atg aag gat gtg aag gtc agc ctc ttc      528
80 Ala Tyr His Ile Thr Val Tyr Met Lys Asp Val Lys Val Ser Leu Phe
81          165          170          175
83 aag aag gac aag gct atg ctc ttc acc tat gat cag tac cag gaa aat      576
84 Lys Lys Asp Lys Ala Met Leu Phe Thr Tyr Asp Gln Tyr Gln Glu Asn
85          180          185          190
87 aat gtg gac cag gcc tcc ggc tct gtg ctc ctg cat ctg gag gtg ggc      624
88 Asn Val Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu Glu Val Gly
89          195          200          205
91 gac caa gtc tgg ctc cag gtg tat ggg gaa gga gag cgt aat gga ctc      672
92 Asp Gln Val Trp Leu Gln Val Tyr Gly Glu Gly Glu Arg Asn Gly Leu
93          210          215          220
95 tat gct gat aat gac aat gac tcc acc ttc aca ggc ttt ctt ctc tac      720
96 Tyr Ala Asp Asn Asp Asn Asp Ser Thr Phe Thr Gly Phe Leu Leu Tyr
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116          20          25          30
119 Lys Gly Ala Cys Thr Gly Trp Met Ala Gly Ile Pro Gly His Pro Gly
120          35          40          45
123 His Asn Gly Ala Pro Gly Arg Asp Gly Arg Asp Gly Thr Pro Gly Glu
124          50          55          60
127 Lys Gly Glu Lys Gly Asp Pro Gly Leu Ile Gly Pro Lys Gly Asp Ile
128 65          70          75          80
131 Gly Glu Thr Gly Val Pro Gly Ala Glu Gly Pro Arg Gly Phe Pro Gly
132          85          90          95
135 Ile Gln Gly Arg Lys Gly Glu Pro Gly Glu Gly Ala Tyr Val Tyr Arg
136          100          105          110
139 Ser Ala Phe Ser Val Gly Leu Glu Thr Tyr Val Thr Ile Pro Asn Met

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140          115          120          125
143 Pro Ile Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn His Tyr Asp
144          130          135          140
147 Gly Ser Thr Gly Lys Phe His Cys Asn Ile Pro Gly Leu Tyr Tyr Phe
148 145          150          155          160
151 Ala Tyr His Ile Thr Val Tyr Met Lys Asp Val Lys Val Ser Leu Phe
152          165          170          175
155 Lys Lys Asp Lys Ala Met Leu Phe Thr Tyr Asp Gln Tyr Gln Glu Asn
156          180          185          190
159 Asn Val Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu Glu Val Gly
160          195          200          205
163 Asp Gln Val Trp Leu Gln Val Tyr Gly Glu Gly Glu Arg Asn Gly Leu
164          210          215          220
167 Tyr Ala Asp Asn Asp Asn Asp Ser Thr Phe Thr Gly Phe Leu Leu Tyr
168 225          230          235          240
171 His Asp Thr Asn
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176 <211> LENGTH: 1276
177 <212> TYPE: DNA
178 <213> ORGANISM: Mus musculus
181 <220> FEATURE:
182 <221> NAME/KEY: CDS
183 <222> LOCATION: (46)..(789)
185 <400> SEQUENCE: 3
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190 caa gct ctc ctg ttc ctc tta atc ctg ccc agt cat gcc gaa gat gac      105
191 Gln Ala Leu Leu Phe Leu Leu Ile Leu Pro Ser His Ala Glu Asp Asp
192 5          10          15          20
194 gtt act aca act gaa gag cta gct cct gct ttg gtc cct cca ccc aag      153
195 Val Thr Thr Thr Glu Leu Ala Pro Ala Leu Val Pro Pro Pro Lys
196          25          30          35
198 gga act tgt gca ggt tgg atg gca ggc atc cca gga cat cct ggc cac      201
199 Gly Thr Cys Ala Gly Trp Met Ala Gly Ile Pro Gly His Pro Gly His
200          40          45          50
202 aat ggc aca cca ggc cgt gat ggc aga gat ggc act cct gga gag aag      249
203 Asn Gly Thr Pro Gly Arg Asp Gly Arg Asp Gly Thr Pro Gly Glu Lys
204          55          60          65
206 gga gag aaa gga gat gca ggt ctt ctt ggt cct aag ggt gag aca gga      297
207 Gly Glu Lys Gly Asp Ala Gly Leu Leu Gly Pro Lys Gly Glu Thr Gly
208          70          75          80
210 gat gtt gga atg aca gga gct gaa ggg cca cgg ggc ttc ccc gga acc      345
211 Asp Val Gly Met Thr Gly Ala Glu Gly Pro Arg Gly Phe Pro Gly Thr
212 85          90          95          100
214 cct ggc agg aaa gga gag cct gga gaa gcc gct tat atg tat cgc tca      393
215 Pro Gly Arg Lys Gly Glu Pro Gly Glu Ala Ala Tyr Met Tyr Arg Ser
216          105          110          115
218 gcg ttc agt gtg ggg ctg gag acc cgc gtc act gtt ccc aat gta ccc      441

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219 Ala Phe Ser Val Gly Leu Glu Thr Arg Val Thr Val Pro Asn Val Pro
220      120      125      130
222 att cgc ttt act aag atc ttc tac aac caa cag aat cat tat gac ggc      489
223 Ile Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn His Tyr Asp Gly
224      135      140      145
226 agc act ggc aag ttc tac tgc aac att ccg gga ctc tac tac ttc tct      537
227 Ser Thr Gly Lys Phe Tyr Cys Asn Ile Pro Gly Leu Tyr Tyr Phe Ser
228      150      155      160
230 tac cac atc acg gtg tac atg aaa gat gtg aag gtg agc ctc ttc aag      585
231 Tyr His Ile Thr Val Tyr Met Lys Asp Val Lys Val Ser Leu Phe Lys
232 165      170      175      180
234 aag gac aag gcc gtt ctc ttc acc tac gac cag tat cag gaa aag aat      633
235 Lys Asp Lys Ala Val Leu Phe Thr Tyr Asp Gln Tyr Gln Glu Lys Asn
236      185      190      195
238 gtg gac cag gcc tct ggc tct gtg ctc ctc cat ctg gag gtg gga gac      681
239 Val Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu Glu Val Gly Asp
240      200      205      210
242 caa gtc tgg ctc cag gtg tat ggg gat ggg gac cac aat gga ctc tat      729
243 Gln Val Trp Leu Gln Val Tyr Gly Asp Gly Asp His Asn Gly Leu Tyr
244      215      220      225
246 gca gat aac gtc aac gac tct aca ttt act ggc ttt ctt ctc tac cat      777
247 Ala Asp Asn Val Asn Asp Ser Thr Phe Thr Gly Phe Leu Leu Tyr His
248      230      235      240
250 gat acc aac tga ctgcaactac ccatagccca tacaccagga gaatcatgga      829
251 Asp Thr Asn
252 245
254 acagtcgaca cactttcagc ttagtttgag agattgattt tattgcttag tttgagagtc      889
256 ctgagtatta tccacacgtg tactcacttg ttcattaaac gactttataa aaaataattt      949
258 gtgttcctag tccagaaaaa aaggcactcc ctgggtctcca cgactcttac atggttagcaa      1009
260 taacagaatg aaaatcacat ttggtatggg ggcttcacaa tattcgcatg actgtctgga      1069
262 agtagaccat gctatttttc tgctcactgt acacaaatat tgttcacata aaccctataa      1129
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272 <211> LENGTH: 247
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279 1      5      10      15
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283      20      25      30
286 Pro Pro Pro Lys Gly Thr Cys Ala Gly Trp Met Ala Gly Ile Pro Gly
287      35      40      45
290 His Pro Gly His Asn Gly Thr Pro Gly Arg Asp Gly Arg Asp Gly Thr
291      50      55      60
294 Pro Gly Glu Lys Gly Glu Lys Gly Asp Ala Gly Leu Leu Gly Pro Lys
295 65      70      75      80

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298 Gly Glu Thr Gly Asp Val Gly Met Thr Gly Ala Glu Gly Pro Arg Gly
299      85      90      95
302 Phe Pro Gly Thr Pro Gly Arg Lys Gly Glu Pro Gly Glu Ala Ala Tyr
303      100      105      110
306 Met Tyr Arg Ser Ala Phe Ser Val Gly Leu Glu Thr Arg Val Thr Val
307      115      120      125
310 Pro Asn Val Pro Ile Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn
311      130      135      140
314 His Tyr Asp Gly Ser Thr Gly Lys Phe Tyr Cys Asn Ile Pro Gly Leu
315 145      150      155      160
318 Tyr Tyr Phe Ser Tyr His Ile Thr Val Tyr Met Lys Asp Val Lys Val
319      165      170      175
322 Ser Leu Phe Lys Lys Asp Lys Ala Val Leu Phe Thr Tyr Asp Gln Tyr
323      180      185      190
326 Gln Glu Lys Asn Val Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu
327      195      200      205
330 Glu Val Gly Asp Gln Val Trp Leu Gln Val Tyr Gly Asp Gly Asp His
331      210      215      220
334 Asn Gly Leu Tyr Ala Asp Asn Val Asn Asp Ser Thr Phe Thr Gly Phe
335 225      230      235      240
338 Leu Leu Tyr His Asp Thr Asn
339      245

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VERIFICATION SUMMARY

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